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PCT09

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/830,144

DATE: 08/30/2001

TIME: 06:24:59

Input Set : A:\06501-076001.txt

Output Set: N:\CRF3\08292001\I830144.raw

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4 <110> APPLICANT: Tsuchiya, Masayuki  
 5 Ohtomo, Toshihiko  
 6 Sugamata, Yasuhiro  
 7 Matsumoto, Kunihiro  
 9 <120> TITLE OF INVENTION: Method for screening compounds inhibiting signal  
 10 transduction through inflammatory cytokines  
 12 <130> FILE REFERENCE: 06501-076001  
 14 <140> CURRENT APPLICATION NUMBER: 09/830,144  
 15 <141> CURRENT FILING DATE: 2001-04-20  
 17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/05817  
 18 <151> PRIOR FILING DATE: 1999-10-21  
 20 <150> PRIOR APPLICATION NUMBER: JP 10/299962  
 21 <151> PRIOR FILING DATE: 1998-10-21  
 23 <160> NUMBER OF SEQ ID NOS: 10  
 25 <170> SOFTWARE: PatentIn version 2.0  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 2656  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Homo sapiens  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (183)..(1919)  
 36 <400> SEQUENCE: 1  
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 41 ggggtctcacc cggattgtcc ggggtggcacc gttcccggcc ccaccgggcg ccgcgaggga 180  
 43 tc atg tct aca gcc tct gcc gcc tcc tcc tcc tcc tcc tcc tcc gcc 227  
 44 Met Ser Thr Ala Ser Ala Ala Ser Ser Ser Ser Ser Ser Ser Ala  
 45 1 5 10 15  
 47 ggt gag atg atc gaa gcc cct tcc cag gtc ctc aac ttt gaa gag atc 275  
 48 Gly Glu Met Ile Glu Ala Pro Ser Gln Val Leu Asn Phe Glu Glu Ile  
 49 20 25 30  
 51 gac tac aag gag atc gag gtg gaa gag gtt gtt gga aga gga gcc ttt 323  
 52 Asp Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe  
 53 35 40 45  
 55 gga gtt gtt tgc aaa gct aag tgg aga gca aaa gat gtt gct att aaa 371  
 56 Gly Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys  
 57 50 55 60  
 59 caa ata gaa agt gaa tct gag agg aaa gcg ttt att gta gag ctt cgg 419  
 60 Gln Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg  
 61 65 70 75  
 63 cag tta tcc cgt gtg aac cat cct aat att gta aag ctt tat gga gcc 467  
 64 Gln Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala  
 65 80 85 90 95  
 67 tgc ttg aat cca gtg tgt ctt gtg atg gaa tat gct gaa ggg ggc tct 515  
 68 Cys Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser  
 69 100 105 110

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71 tta tat aat gtg ctg cat ggt gct gaa cca ttg cca tat tat act gct      563
72 Leu Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala
73      115      120      125
75 gcc cac gca atg agt tgg tgt tta cag tgt tcc caa gga gtg gct tat      611
76 Ala His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr
77      130      135      140
79 ctt cac agc atg caa ccc aaa gcg cta att cac agg gac ctg aaa cca      659
80 Leu His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro
81      145      150      155
83 cca aac tta ctg ctg gtt gca ggg ggg aca gtt cta aaa att tgt gat      707
84 Pro Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp
85 160      165      170      175
87 ttt ggt aca gcc tgt gac att cag aca cac atg acc aat aac aag ggg      755
88 Phe Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly
89      180      185      190
91 agt gct gct tgg atg gca cct gaa gtt ttt gaa ggt agt aat tac agt      803
92 Ser Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser
93      195      200      205
95 gaa aaa tgt gac gtc ttc agc tgg ggt att att ctt tgg gaa gtg ata      851
96 Glu Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile
97      210      215      220
99 acg cgt cgg aaa ccc ttt gat gag att ggt ggc cca gct ttc cga atc      899
100 Thr Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile
101      225      230      235
103 atg tgg gct gtt cat aat ggt act cga cca cca ctg ata aaa aat tta      947
104 Met Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu
105 240      245      250      255
107 cct aag ccc att gag agc ctg atg act cgt tgt tgg tct aaa gat cct      995
108 Pro Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro
109      260      265      270
111 tcc cag cgc cct tca atg gag gaa att gtg aaa ata atg act cac ttg      1043
112 Ser Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu
113      275      280      285
115 atg cgg tac ttt cca gga gca gat gag cca tta cag tat cct tgt cag      1091
116 Met Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln
117      290      295      300
119 tat tca gat gaa gga cag agc aac tct gcc acc agt aca ggc tca ttc      1139
120 Tyr Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe
121      305      310      315
123 atg gac att gct tct aca aat acg agt aac aaa agt gac act aat atg      1187
124 Met Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met
125 320      325      330      335
127 gag caa gtt cct gcc aca aat gat act att aag cgc tta gaa tca aaa      1235
128 Glu Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys
129      340      345      350
131 ttg ttg aaa aat cag gca aag caa cag agt gaa tct gga cgt tta agc      1283
132 Leu Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser
133      355      360      365
135 ttg gga gcc tcc cat ggg agc agt gtg gag agc ttg ccc cca acc tct      1331

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136 Leu Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser
137          370          375          380
139 gag ggc aag agg atg agt gct gac atg tct gaa ata gaa gct agg atc 1379
140 Glu Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile
141          385          390          395
143 gcc gca acc aca ggc aac gga cag cca aga cgt aga tcc atc caa gac 1427
144 Ala Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp
145 400          405          410          415
147 ttg act gta act gga aca gaa cct ggt cag gtg agc agt agg tca tcc 1475
148 Leu Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser
149          420          425          430
151 agt ccc agt gtc aga atg att act acc tca gga cca acc tca gaa aag 1523
152 Ser Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys
153          435          440          445
155 cca act cga agt cat cca tgg acc cct gat gat tcc aca gat acc aat 1571
156 Pro Thr Arg Ser His Pro Trp Thr Thr Pro Asp Asp Ser Thr Asp Thr Asn
157          450          455          460
159 gga tca gat aac tcc atc cca atg gct tat ctt aca ctg gat cac caa 1619
160 Gly Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln
161          465          470          475
163 cta cag cct cta gca ccg tgc cca aac tcc aaa gaa tct atg gca gtg 1667
164 Leu Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val
165 480          485          490          495
167 ttt gaa cag cat tgt aaa atg gca caa gaa tat atg aaa gtt caa aca 1715
168 Phe Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr
169          500          505          510
171 gaa att gca ttg tta tta cag aga aag caa gaa cta gtt gca gaa ctg 1763
172 Glu Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu
173          515          520          525
175 gac cag gat gaa aag gac cag caa aat aca tct cgc ctg gta cag gaa 1811
176 Asp Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu
177          530          535          540
179 cat aaa aag ctt tta gat gaa aac aaa agc ctt tct act tac tac cag 1859
180 His Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln
181          545          550          555
183 caa tgc aaa aaa caa cta gag gtc atc aga agt cag cag cag aaa cga 1907
184 Gln Cys Lys Lys Gln Leu Glu Val Ile Arg Ser Gln Gln Gln Lys Arg
185 560          565          570          575
187 caa ggc act tca tgattctctg ggaccgttac attttgaaat atgcaaagaa 1959
188 Gln Gly Thr Ser
191 agactttttt tttaaggaaa ggaaaacctt ataatgacga ttcattgagt ttagcttttt 2019
193 ggcgtgttct gaatgccaac tgccatatatt tgcgtgcat ttttcattgt ttattttcct 2079
195 tttctcatgg tggacataca attttactgt ttcattgcat aacatggtag catctgtgac 2139
197 ttgaatgagc agcactttgc aacttcaaaa cagatgcagt gaactgtggc tgtatatgca 2199
199 tgctcattgt gtgaaggcta gcctaacaga acaggaggta tcaaactagc tgctatgtgc 2259
201 aaacagcgtc cattttttca tattagaggt ggaacctcaa gaatgacttt attcttgtat 2319
203 ctcatctcaa aatattaata atttttttcc caaagatgg tatataccaa gttaaagaca 2379
205 gggattata aatttagagt gattgggtgg atattacgga aatacggaac ctttagggat 2439
207 agttccgtgt aagggttttg atgccagcat ccttggtatca gtactgaact cagttccatc 2499

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228 Tyr Lys Glu Ile Glu Val Glu Glu Val Val Gly Arg Gly Ala Phe Gly
229 35 40 45
231 Val Val Cys Lys Ala Lys Trp Arg Ala Lys Asp Val Ala Ile Lys Gln
232 50 55 60
234 Ile Glu Ser Glu Ser Glu Arg Lys Ala Phe Ile Val Glu Leu Arg Gln
235 65 70 75 80
237 Leu Ser Arg Val Asn His Pro Asn Ile Val Lys Leu Tyr Gly Ala Cys
238 85 90 95
240 Leu Asn Pro Val Cys Leu Val Met Glu Tyr Ala Glu Gly Gly Ser Leu
241 100 105 110
243 Tyr Asn Val Leu His Gly Ala Glu Pro Leu Pro Tyr Tyr Thr Ala Ala
244 115 120 125
246 His Ala Met Ser Trp Cys Leu Gln Cys Ser Gln Gly Val Ala Tyr Leu
247 130 135 140
249 His Ser Met Gln Pro Lys Ala Leu Ile His Arg Asp Leu Lys Pro Pro
250 145 150 155 160
252 Asn Leu Leu Leu Val Ala Gly Gly Thr Val Leu Lys Ile Cys Asp Phe
253 165 170 175
255 Gly Thr Ala Cys Asp Ile Gln Thr His Met Thr Asn Asn Lys Gly Ser
256 180 185 190
258 Ala Ala Trp Met Ala Pro Glu Val Phe Glu Gly Ser Asn Tyr Ser Glu
259 195 200 205
261 Lys Cys Asp Val Phe Ser Trp Gly Ile Ile Leu Trp Glu Val Ile Thr
262 210 215 220
264 Arg Arg Lys Pro Phe Asp Glu Ile Gly Gly Pro Ala Phe Arg Ile Met
265 225 230 235 240
267 Trp Ala Val His Asn Gly Thr Arg Pro Pro Leu Ile Lys Asn Leu Pro
268 245 250 255
270 Lys Pro Ile Glu Ser Leu Met Thr Arg Cys Trp Ser Lys Asp Pro Ser
271 260 265 270
273 Gln Arg Pro Ser Met Glu Glu Ile Val Lys Ile Met Thr His Leu Met
274 275 280 285
276 Arg Tyr Phe Pro Gly Ala Asp Glu Pro Leu Gln Tyr Pro Cys Gln Tyr
277 290 295 300
279 Ser Asp Glu Gly Gln Ser Asn Ser Ala Thr Ser Thr Gly Ser Phe Met
280 305 310 315 320
282 Asp Ile Ala Ser Thr Asn Thr Ser Asn Lys Ser Asp Thr Asn Met Glu

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283          325          330          335
285 Gln Val Pro Ala Thr Asn Asp Thr Ile Lys Arg Leu Glu Ser Lys Leu
286          340          345          350
288 Leu Lys Asn Gln Ala Lys Gln Gln Ser Glu Ser Gly Arg Leu Ser Leu
289          355          360          365
291 Gly Ala Ser His Gly Ser Ser Val Glu Ser Leu Pro Pro Thr Ser Glu
292          370          375          380
294 Gly Lys Arg Met Ser Ala Asp Met Ser Glu Ile Glu Ala Arg Ile Ala
295 385          390          395          400
297 Ala Thr Thr Gly Asn Gly Gln Pro Arg Arg Arg Ser Ile Gln Asp Leu
298          405          410          415
300 Thr Val Thr Gly Thr Glu Pro Gly Gln Val Ser Ser Arg Ser Ser
301          420          425          430
303 Pro Ser Val Arg Met Ile Thr Thr Ser Gly Pro Thr Ser Glu Lys Pro
304          435          440          445
306 Thr Arg Ser His Pro Trp Thr Pro Asp Asp Ser Thr Asp Thr Asn Gly
307          450          455          460
309 Ser Asp Asn Ser Ile Pro Met Ala Tyr Leu Thr Leu Asp His Gln Leu
310 465          470          475          480
312 Gln Pro Leu Ala Pro Cys Pro Asn Ser Lys Glu Ser Met Ala Val Phe
313          485          490          495
315 Glu Gln His Cys Lys Met Ala Gln Glu Tyr Met Lys Val Gln Thr Glu
316          500          505          510
318 Ile Ala Leu Leu Leu Gln Arg Lys Gln Glu Leu Val Ala Glu Leu Asp
319          515          520          525
321 Gln Asp Glu Lys Asp Gln Gln Asn Thr Ser Arg Leu Val Gln Glu His
322          530          535          540
324 Lys Lys Leu Leu Asp Glu Asn Lys Ser Leu Ser Thr Tyr Tyr Gln Gln
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335 <211> LENGTH: 1560
336 <212> TYPE: DNA
337 <213> ORGANISM: Homo sapiens
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348 ctg cag agt gag cag cag cca agc tgg aca gat gac ctg cct ctc tgc      101
349 Leu Gln Ser Glu Gln Gln Pro Ser Trp Thr Asp Asp Leu Pro Leu Cys
350          10          15          20
352 cac ctc tct ggg gtt ggc tca gcc tcc aac cgc agc tac tct gct gat      149
353 His Leu Ser Gly Val Gly Ser Ala Ser Asn Arg Ser Tyr Ser Ala Asp
354 25          30          35          40

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**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/830,144

DATE: 08/30/2001

TIME: 06:25:00

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